

Database : PIR\_78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result      Query

No.	Score	Match	Length	DB	ID	Description
1	1693	99.7	365	2	A43720	parathion hydrolas
2	913	53.8	325	2	A28214	phosphotriesterase
3	448	26.4	326	2	D70962	hypothetical prote
4	408	24.0	314	2	F90424	hypothetical prote
5	385	22.7	323	2	E75459	probable phosphotr
6	331	19.5	305	2	AB1321	probable phosphotr
7	309	18.2	331	2	A83678	hypothetical prote
8	308	18.1	292	2	F65132	hypothetical 32.9
9	296	17.4	679	2	F83723	hypothetical prote
10	277.5	16.3	355	2	AD2933	hypothetical prote
11	277.5	16.3	355	2	C98349	resiniferatoxin-bi
12	273	16.1	344	2	AC0994	puative phophotrie
13	269.5	15.9	330	2	AG1405	Phosphotriesterase
14	268.5	15.8	330	2	AG1781	Phosphotriesterase
15	229	13.5	351	2	A99586	conserved hypothet

RESULT 1

A43720

parathion hydrolase precursor - Flavobacterium sp. (ATCC 27551)

C;Species: Flavobacterium sp.

C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 08-Oct-1999

C;Accession: A43720

R;Mulbry, W.W.; Karns, J.S.

J. Bacteriol. 171, 6740-6746, 1989

A;Title: Parathion hydrolase specified by the Flavobacterium opd gene: relationship between the gene and protein.

A;Reference number: A43720; MUID:90078122; PMID:2556372

A;Accession: A43720

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-365 <MUL>

A;Cross-references: GB:M29593; NID:g148712; PIDN:AAA24930.1; PID:g148713

A;Experimental source: ATCC 27551

Query Match 99.7%; Score 1693; DB 2; Length 365;

Best Local Similarity 100.0%; Pred. No. 1.1e-126;

Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2

SIGTGDRINTVRGPITISEAGFTLTHEHICSSAGFLRAWPEFFGSRKALAEKAVRGLRR  
61

||||||||||||||||||||||||||||||

Db 30

SIGTGDRINTVRGPITISEAGFTLTHEHICSSAGFLRAWPEFFGSRKALAEKAVRGLRR  
89

Qy 62

ARAAGVRTIVDVSTFDIGRDVSLLAEVSRADVHIVAATGLWFDPPLSMRLRSVEELTQF  
121

||||||||||||||||||||||||||

Db 90

ARAAGVRTIVDVSTFDIGRDVSLLAEVSRADVHIVAATGLWFDPPLSMRLRSVEELTQF  
149

Qy 122

FLREIQYGIEDTGIRAGIIVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG  
181

|||||||

Db 150

FLREIQYGIEDTGIRAGIIVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG  
209

Qy 182

EQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS  
241

|||||||

Db 210

EQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS  
269

Qy 242

ALLGIRSWQTRALLIKALIDQGYMKQILVSNDLFGFSSYVTNIMDVMDRVNPDGMAFIP  
301

|||||||

Db 270

ALLGIRSWQTRALLIKALIDQGYMKQILVSNDLFGFSSYVTNIMDVMDRVNPDGMAFIP  
329

Qy 302 LRVIPFLREKGVPQETLAGITVTNPARFLSPTLRAS 337

|||||||

Db 330 LRVIPFLREKGVPQETLAGITVTNPARFLSPTLRAS 365

Database : A\_Geneseq\_29Jan04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	1695	99.8	337	5	ABB79958	Abb79958 Organopho
2	1693	99.7	336	6	ABG72651	Abg72651 Flavobact
3	1693	99.7	365	2	AAR05573	Aar05573 Parathion
4	1693	99.7	365	6	ABB82802	Abb82802 Flavobact
5	1689	99.5	336	6	ABG72650	Abg72650 Flavobact
6	1686	99.3	357	2	AAY43487	Aay43487 Amino aci
7	1685	99.2	334	2	AAY43486	Aay43486 Amino aci
8	1558	91.8	356	6	ABB82799	Abb82799 A. radiob
9	1558	91.8	384	6	ABB82798	Abb82798 A. radiob
10	1552	91.4	384	6	ABB82801	Abb82801 A. radiob
11	1535	90.4	384	6	ABB82800	Abb82800 A. radiob
12	465	27.4	326	6	ABU33918	Abu33918 Protein e
13	448	26.4	326	6	ABU36432	Abu36432 Protein e
14	400	23.6	306	6	ABU34486	Abu34486 Protein e
15	372.5	21.9	346	6	ABU31613	Abu31613 Protein e
16	331	19.5	305	5	ABB48499	Abb48499 Listeria
17	331	19.5	305	6	ABU32460	Abu32460 Protein e
18	308	18.1	292	6	ABU14978	Abu14978 Protein e
19	283	16.7	345	6	ABU21704	Abu21704 Protein e
20	273	16.1	344	6	ABU47684	Abu47684 Protein e
21	273	16.1	344	6	ABU47288	Abu47288 Protein e
22	269.5	15.9	330	5	ABB47719	

RESULT 1  
ABB79958  
ID ABB79958 standard; protein; 337 AA.  
XX  
AC ABB79958;  
XX  
DT 12-DEC-2002 (first entry)  
XX  
DE Organophosphorous hydrolase.  
XX  
KW Organophosphorous hydrolase; OPH; enzyme; immobilisation;  
KW chemical warfare; pesticide; pollutant; detoxification; decontamination.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1. .29  
FT /label= Signal\_peptide  
FT Protein 30. .337  
FT /label= Mature\_protein  
XX  
PN WO200268454-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 21-FEB-2002; 2002WO-US005755.  
XX  
PR 21-FEB-2001; 2001US-00791138.  
PR 20-FEB-2002; 2002US-00081737.  
XX  
PA (BATT ) BATTELLE MEMORIAL INST.  
XX  
PI Ackerman EJ, Liu J, Chenghong L;  
XX  
DR WPI; 2002-713364/77.  
DR N-PSDB; ABQ81428.  
XX  
PT Protein system, for facilitating chemical reactions e.g. hydrolysis,  
PT oxidation, hydrogenation and proteolysis, comprises porous matrix  
PT material and protein within matrix.  
XX  
PS Example; Fig 4; 56pp; English.  
XX  
CC The present sequence is the protein sequence of an organophosphorous  
CC hydrolase (OPH) encoded by an expression plasmid of the invention. The  
CC invention provides a method for producing OPH by transfecting a host cell  
CC with a vector comprising a sequence encoding OPH linked to a T7  
CC expression control sequence, culturing the transfected host cell, and  
CC purifying OPH from the cell or culture medium. This OPH has an activity  
CC of about 13,000 U/mg. The host cell can be prokaryotic, e.g. Escherichia  
CC coli, or eukaryotic, e.g. Pichia pastoris. The invention also provides a  
CC protein system for facilitating chemical reactions. The protein system  
CC comprises a porous matrix material having a pore volume of which at least  
CC 90% is composed of pores of 50-400 Angstroms. The protein occupies 5-40%  
CC of the average pore volume, and is preferably an enzyme, especially OPH  
CC having an activity of 60-95% that of the active state and retaining about  
CC 10% of its activity after 24 hr under alkaline conditions. The porous

CC matrix may comprise surface hydroxyls that are reacted with a coupling  
CC agent to form a functionalised monolayer. The system provides high enzyme  
CC activities on a porous support, stability under a variety of conditions,  
CC high densities of active protein and capability in industrial-scale  
CC applications. It provides environmentally safe methods of destroying  
CC chemical weapons and organophosphorous pesticides while avoiding the  
CC dangers inherent in burning these materials. It can be used in filtration  
CC equipment for individual soldiers and pesticide workers, and in vehicles,  
CC aircraft, ships and buildings such as civilian and military defence  
CC shelters, to perform detoxifications

XX

SQ Sequence 337 AA;

Query Match 99.8%; Score 1695; DB 5; Length 337;  
Best Local Similarity 99.7%; Pred. No. 1.1e-163;  
Matches 336; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSIGTGDRINTVRGPITISEAGFTLTTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLR 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MSIGTGDRINTVRGPITISEAGFTLTTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLR 60

Qy 61 RARAAGVRTIVDVSTFDIGRDVSLLAEVSRAADVHIVATGLWFDPLSMLRSVEELTQ 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 RARAAGVRTIVDVSTFDIGRDVSLLAEVSRAADVHIVATGLWFDPLSMLRSVEELTQ 120

Qy 121 FFLREIQtyGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTHTAASQRD 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 FFLREIQtyGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTHTAASQRD 180

Qy 181 GEQQAAIFESEGLSPSRVCIGHSDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASA 240  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 GEQQAAIFESEGLSPSRVCIGHSDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASA 240

Qy 241 SALLGIRSWQTRALLIKALIDQGYMKQILVSNDLFGFSSYVTNIMDVMDRVNPDGMAFI 300  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 241 SALLGIRSWQTRALLIKALIDQGYMKQILVSNDLFGFSSYVTNIMDVMDRVNPDGMAFI 300

Qy 301 PLRVI PFLREKGVPQETLAGITVTNPARFLSPTLRAS 337

||| ||| ||| : ||| ||| ||| ||| ||| |||

Db 301 PLRVI PFLREKGVPQQTLAGITVTNPARFLSPTLRAS 337

Database : SPTREMBL\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rat:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query				Description
	Score	Match	Length	DB ID	
1	1688	99.4	365	2 Q8GC45	Q8gc45 flavobacter
2	1630	96.0	365	2 Q8VLR0	Q8vlr0 chryseobact
3	1558	91.8	384	2 Q93LD7	Q93ld7 agrobacteri
4	915	53.9	325	2 Q47934	Q47934 flavobacter
5	448	26.4	326	16 Q7U2I4	Q7u2i4 mycobacteri
6	408	24.0	314	17 Q97VT7	Q97vt7 sulfolobus
7	385	22.7	323	16 Q9RVU2	Q9rvu2 deinococcus
8	331	19.5	305	16 Q8Y5T5	Q8y5t5 listeria mo
9	325.5	19.2	362	16 Q985I1	Q985i1 rhizobium l
10	309	18.2	331	16 Q9KG87	Q9kg87 bacillus ha
11	306	18.0	292	16 Q8FCW5	Q8fcw5 escherichia
12	304	17.9	292	16 Q7UAS1	Q7uas1 shigella fl
13	296	17.4	679	16 Q9KF95	Q9kf95 bacillus ha
14	288	17.0	344	16 Q8FG90	Q8fg90 escherichia
15	277.5	16.3	355	16 Q8UBF0	Q8ubf0 agrobacteri
16	273	16.1	344	16 Q8XFU6	Q8xfu6 salmonella
17	270.5	15.9	349	13 Q7Szs2	Q7szs2 xenopus lae
18	269.5	15.9	330	16 Q8Y427	Q8y427 listeria mo
19	268.5	15.8	330	16 Q927J1	Q927j1 listeria in

RESULT 1

Q8GC45

ID Q8GC45 PRELIMINARY; PRT; 365 AA.  
AC Q8GC45;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Parathion hydrolase precursor (EC 3.1.8.1).  
GN OPD.  
OS Flavobacterium sp. ATCC 27551.  
OG Plasmid pPDL2.  
OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;  
OC Flavobacteriaceae; Flavobacterium.  
OX NCBI\_TaxID=74567;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 27551;  
RA Siddavatam D., Manavathi B., Merrick M.;  
RT "The conserved region surrounding the organophosphorus pesticide  
degrading (opd) gene on the Flavobacterium plasmid pPDL2 has the  
features of a complex transposon."  
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AJ421424; CAD13181.1; -.  
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
DR GO; GO:0004063; F:aryldialkylphosphatase activity; IEA.  
DR GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0009056; P:catabolism; IEA.  
DR InterPro; IPR000437; Prok\_lipoprot\_S.  
DR InterPro; IPR001559; PTE.  
DR Pfam; PF02126; PTE; 1.  
DR PROSITE; PS01322; PHOSPHOTRIESTERASE\_1; 1.  
DR PROSITE; PS01323; PHOSPHOTRIESTERASE\_2; 1.  
DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
KW Signal; Hydrolase; Plasmid.  
FT SIGNAL 1 29  
SQ SEQUENCE 365 AA; 38973 MW; 0C92FE577BFE4FB0 CRC64;

Query Match 99.4%; Score 1688; DB 2; Length 365;  
Best Local Similarity 99.7%; Pred. No. 8.6e-124;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SIGTGDRINTVRGPITISEAGFTLTTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR 61  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 30 SIGTGDRINTVRGPITISEAGFTLTTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR 89

Qy 62 ARAAGVRTIVDVSTFDIGRDVSLLAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQF 121  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 90 ARAAGVRTIVDVSTFDIGRDVSLLAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQF 149

Qy 122 FLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG 181  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 150 FLREIQYGIEDTGIRAGIIKVATTGKAAPFQELVLKAAARASLATGVPVTTHTAASQRDG 209

Qy 182 EQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS 241  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 210 EQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS 269

Qy 242 ALLGIRSWQTRALLIKALIDQGYMKQILVSNDLFGFSSYVTNIMDVMDRVNPDGMAFIP 301  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 270 ALLGIRSWQTRALLIKALIDQGYMKQILVSNDLFGFSSYVTNIMDVMDRVNPDGMAFIP 329

Qy 302 LRVIPFLREKGVPQETLAGITVTNPARFLSPTLRAS 337  
||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 330 LRVIPFLREKGVPQETLAGITVTNPARFLSPTLRAS 365

RESULT 2

Q8VLR0

ID Q8VLR0 PRELIMINARY; PRT; 365 AA.  
AC Q8VLR0;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Parathion hydrolase precursor (EC 3.1.8.1).  
GN OPD.  
OS Chryseobacterium balustinum.  
OG Plasmid pBC9.  
OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;  
OC Flavobacteriaceae; Chryseobacterium.  
OX NCBI\_TaxID=246;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Siddavatam D., Manavathi B., Merrick M.;  
RT "The conserved region surrounding the organophosphorus pesticide  
degrading (opd) gene on the *Flavobacterium* plasmid pPDL2 has the  
features of a complex transposon."  
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AJ426431; CAD19996.1; -.  
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
DR GO; GO:0004063; F:aryldialkylphosphatase activity; IEA.  
DR GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0009056; P:catabolism; IEA.  
DR InterPro; IPR001559; PTE.  
DR Pfam; PF02126; PTE; 1.  
DR PROSITE; PS01322; PHOSPHOTRIESTERASE\_1; 1.  
DR PROSITE; PS01323; PHOSPHOTRIESTERASE\_2; 1.  
KW Signal; Hydrolase; Plasmid.  
FT SIGNAL 1 29 POTENTIAL.  
FT CHAIN 30 365 PARATHION HYDROLASE.  
SQ SEQUENCE 365 AA; 39116 MW; AA9EC0E3BDD3F811 CRC64;  
  
Query Match 96.0%; Score 1630; DB 2; Length 365;  
Best Local Similarity 96.4%; Pred. No. 3e-119;  
Matches 324; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 2 SIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR 61  
||| ||| ||| ||| ||| ||| ||| : ||| ||| ||| ||| ||| ||| |||  
Db 30 SIGTGDRINTVRGPITNSEAGFTLTHEHICGTSAGFLRAWQEFFFGRKALAEKAVRGLRR 89  
  
Qy 62 ARAAGVRTIVDVSTFDIGRDVSLLAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQF 121  
||| ||| ||| ||| ||| ||| ||| ||| ||| : ||| : | ||| ||| ||| : ||| ||| |||  
Db 90 ARAAGVRTIVDVSTFDIGRDVSLLAEVSMMVDVSLLAETGLWFDPPLSIGLRSVEELTQF 149  
  
Qy 122 FLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTHTAASQRDG 181  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 150 FLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTHTAASQRDG 209  
  
Qy 182 EQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHI PHSAIGLEDNASAS 241  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 210 EQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHI PHSAIGLEDNASAS 269  
  
Qy 242 ALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIP 301

Db 270 ||||||| ALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIP 329

Qy 302 LRVIPFLREKGVPQETLAGITVTNPARFLSPTLRAS 337  
|||

Db 330 LRVIPFLREKGVPQETLAGITVTNPARFLSPTLRAS 365

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query				Description
	Score	Match	Length	DB	
1	1689	99.5	,	336	4 US-09-603-450-4 Sequence 4, Appli
2	1688	99.4		365	6 5484728-2 Patent No. 5484728
3	267	15.7		352	4 US-09-543-681A-8100 Sequence 8100, Ap
4	238.5	14.0		349	1 US-08-343-027A-12 Sequence 12, Appl
5	105	6.2		477	4 US-09-489-039A-9937 Sequence 9937, Ap
6	104	6.1		495	4 US-09-252-991A-21509 Sequence 21509, A
7	99.5	5.9		2482	4 US-09-252-991A-16967 Sequence 16967, A
8	92	5.4		908	4 US-09-328-352-7168 Sequence 7168, Ap
9	91.5	5.4		461	4 US-09-134-000C-5551 Sequence 5551, Ap
10	90.5	5.3		647	4 US-09-725-735A-18 Sequence 18, Appl
11	90	5.3		569	4 US-09-543-681A-5106 Sequence 5106, Ap
12	89.5	5.3		1161	4 US-09-252-991A-22872 Sequence 22872, A
13	89	5.2		403	4 US-09-252-991A-25706 Sequence 25706, A
14	89	5.2		655	4 US-09-107-532A-4425 Sequence 4425, Ap
15	88.5	5.2		283	4 US-09-543-681A-8240 Sequence 8240, Ap
16	87	5.1		288	4 US-09-252-991A-18721 Sequence 18721, A
17	87	5.1		476	4 US-09-489-039A-14013 Sequence 14013, A

RESULT 1

US-09-603-450-4

; Sequence 4, Application US/09603450  
; Patent No. 6469145  
; GENERAL INFORMATION:  
; APPLICANT: Rastogi, Vipin K  
; APPLICANT: Cheng, Tu-c  
; APPLICANT: DeFrank, Joseph J  
; TITLE OF INVENTION: One-Step Purification Process for Organophosphorus  
; TITLE OF INVENTION: Hydrolase Enzyme  
; FILE REFERENCE: DAM-508-99  
; CURRENT APPLICATION NUMBER: US/09/603,450  
; CURRENT FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 336  
; TYPE: PRT  
; ORGANISM: Flavobacterium sp

US-09-603-450-4

Query Match 99.5%; Score 1689; DB 4; Length 336;  
Best Local Similarity 100.0%; Pred. No. 4.7e-174;  
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	3	IGTGDRINTVRGPITISEAGFTLT	HEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRRA	62
Db	2	IGTGDRINTVRGPITISEAGFTLT	HEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRRA	61
Qy	63	RAAGVRTIVDVSTFDIGRDVSLLAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQFF	122	
Db	62	RAAGVRTIVDVSTFDIGRDVSLLAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQFF	121	
Qy	123	LREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTHTAASQRDGE	182	
Db	122	LREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTHTAASQRDGE	181	
Qy	183	QQAAIFESEGLSPSRVCIGHSDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASASA	242	
Db	182	QQAAIFESEGLSPSRVCIGHSDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASASA	241	
Qy	243	LLGIRSWQTRALLIKALIDQGYMKQILVSNDLWFGFSSYVTNIMDVMDRVNPDGMAFIPL	302	
Db	242	LLGIRSWQTRALLIKALIDQGYMKQILVSNDLWFGFSSYVTNIMDVMDRVNPDGMAFIPL	301	
Qy	303	RVIPFLREKGVPQETLAGITVTNPARFLSPTLRAS	337	
Db	302	RVIPFLREKGVPQETLAGITVTNPARFLSPTLRAS	336	

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		%	ID	Description
		Match	Length	DB		
1	1693	99.7	365	1	OPD_FLASP	P16648 flavobacter
2	448	26.4	326	1	PHP_MYCTU	P96413 mycobacteri
3	308	18.1	292	1	PHP_ECOLI	P45548 escherichia
4	243.5	14.3	349	1	PTER_HUMAN	Q96bw5 homo sapien
5	242.5	14.3	349	1	PTER_RAT	Q63530 rattus norv
6	239.5	14.1	349	1	PTER_MOUSE	Q60866 mus musculu
7	211.5	12.5	350	1	PTER_DROME	Q9vhf2 drosophila
8	127	7.5	216	1	YE97_MYCPN	P75290 mycoplasma
9	103	6.1	226	1	GPH2_PSEAE	Q9hz62 pseudomonas
10	103	6.1	319	1	HE31_STRCO	Q9wx16 streptomyce
11	96	5.7	342	1	ARGC_STRCO	P54895 streptomyce
12	93.5	5.5	352	1	TFTE_BURCE	Q45072 burkholderi
13	93	5.5	3421	1	TEGU_HSVEB	P28955 equine herp
14	92.5	5.4	522	1	LEU1_DEIRA	Q9rua9 deinococcus
15	92.5	5.4	898	1	SYA_METTH	O27718 methanobact
16	92	5.4	486	1	LE11_PYRAB	Q9uz08 pyrococcus
17	92	5.4	617	1	VATA_MANSE	P31400 manduca sex
18	91.5	5.4	494	1	TYRO_RHIME	P33180 rhizobium m
19	91.5	5.4	520	1	LEU1_YERPE	Q8zig8 yersinia pe
20	91.5	5.4	1139	1	VRNA_BSMV	P17595 barley stri
21	91	5.4	1290	1	RPOC_MYCPN	P75271 mycoplasma
22	90.5	5.3	333	1	YF72_HALN1	Q9hp18 halobacteri
23	90.5	5.3	838	1	GLGB_STRAW	Q82jf0 streptomyce
24	89.5	5.3	300	1	Y505_MYCLE	Q49823 mycobacteri
25	89.5	5.3	308	1	Y505_MYCTU	Q11169 mycobacteri
26	89.5	5.3	435	1	PROA_BRAJA	Q89x85 bradyrhizob
27	89.5	5.3	958	1	GCP2_PSEAE	Q9htx7 pseudomonas
28	89	5.2	614	1	VAA2_DROME	Q27331 drosophila

RESULT 1

OPD\_FLASP

ID OPD\_FLASP STANDARD; PRT; 365 AA.  
AC P16648; P13739;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Parathion hydrolase precursor (EC 3.1.8.1) (Phosphotriesterase)  
(PTE).  
GN OPD.  
OS Flavobacterium sp. (strain ATCC 27551), and  
OS Brevundimonas diminuta (Pseudomonas diminuta).  
OG Plasmid pCMS1.  
OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;  
OC Flavobacteriaceae; Flavobacterium.  
OX NCBI\_TaxID=239, 293;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-53.  
RC SPECIES=Flavobacterium sp ATCC 27551;  
RX MEDLINE=90078122; PubMed=2556372;  
RA Mulbry W.W., Karns J.S.;  
RT "Parathion hydrolase specified by the Flavobacterium opd gene:  
RT relationship between the gene and protein.";  
RL J. Bacteriol. 171:6740-6746(1989).  
RN [2]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-44.  
RC SPECIES=B.diminuta; STRAIN=MG;  
RA Serdar C.M., Murdock D.C., Rohde M.F.;  
RT "Parathion hydrolase gene from Pseudomonas diminuta MG: subcloning,  
RT complete nucleotide sequence, and expression of the mature portion of  
RT the enzyme in Escherichia coli.";  
RL Biotechnology 7:1151-1155(1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES=B.diminuta; STRAIN=MG;  
RX MEDLINE=88198028; PubMed=2834339;  
RA McDaniel C.S., Harper L.L., Wild J.R.;  
RT "Cloning and sequencing of a plasmid-borne gene (opd) encoding a  
RT phosphotriesterase.";  
RL J. Bacteriol. 170:2306-2311(1988).  
RN [4]  
RP ACTIVE SITE.  
RX MEDLINE=94206935; PubMed=8155644;  
RA Kuo J.M., Raushel F.M.;  
RT "Identification of the histidine ligands to the binuclear metal  
RT center of phosphotriesterase by site-directed mutagenesis.";  
RL Biochemistry 33:4265-4272(1994).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RC SPECIES=B.diminuta;  
RX MEDLINE=95092756; PubMed=7999757;  
RA Benning M.M., Kuo J.M., Raushel F.M., Holden H.M.;  
RT "Three-dimensional structure of phosphotriesterase: an enzyme capable  
RT of detoxifying organophosphate nerve agents.";  
RL Biochemistry 33:15001-15007(1994).  
RN [6]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RC SPECIES=B.diminuta;  
RX MEDLINE=95315185; PubMed=7794910;  
RA Benning M.M., Kuo J.M., Raushel F.M., Holden H.M.;  
RT "Three-dimensional structure of the binuclear metal center of  
RT phosphotriesterase.";  
RL Biochemistry 34:7973-7978(1995).  
RN [7]  
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
RC SPECIES=B.diminuta;  
RX MEDLINE=96214508; PubMed=8634243;  
RA Vanhooke J.L., Benning M.M., Raushel F.M., Holden H.M.;  
RT "Three-dimensional structure of the zinc-containing  
RT phosphotriesterase with the bound substrate analog diethyl  
RT 4-methylbenzylphosphonate.";  
RL Biochemistry 35:6020-6025(1996).  
CC -!!- FUNCTION: Has an unusual substrate specificity for synthetic  
CC organophosphate triesters and phosphorofluoridates. All of the  
CC phosphate triesters found to be substrates are synthetic  
CC compounds. The identity of any naturally occurring substrate for  
CC the enzyme is unknown. Has no detectable activity with phosphate  
CC monoesters or diesters and no activity as an esterase or protease.  
CC It catalyzes the hydrolysis of the insecticide paraoxon at a rate  
CC approaching the diffusion limit and thus appears to be optimally  
CC evolved for utilizing this synthetic substrate.  
CC -!!- CATALYTIC ACTIVITY: Aryl dialkyl phosphate + H(2)O = dialkyl  
CC phosphate + an aryl alcohol.  
CC -!!- COFACTOR: Binds 2 zinc ions per subunit.  
CC -!!- PATHWAY: Pesticide detoxification.  
CC -!!- SUBUNIT: Homodimer.  
CC -!!- SUBCELLULAR LOCATION: Membrane-associated.  
CC -!!- BIOTECHNOLOGY: Has attracted interest because of its potential use  
CC in the detoxification of chemical waste and warfare agents and its  
CC ability to degrade agricultural pesticides such as parathion.  
CC -!!- SIMILARITY: Belongs to the phosphotriesterase family.  
CC -!!- CAUTION: Ref.3 sequence differs from that shown due to multiple  
CC sequencing errors.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M29593; AAA24930.1; -  
DR EMBL; M20392; AAA98299.1; ALT\_FRAME.  
DR PIR; A28214; A28214.  
DR PIR; A43720; A43720.  
DR PDB; 1DPM; 20-AUG-97.  
DR PDB; 1EYW; 20-DEC-00.  
DR PDB; 1EZ2; 20-DEC-00.  
DR PDB; 1HZY; 04-APR-01.  
DR PDB; 1I0B; 04-APR-01.  
DR PDB; 1I0D; 04-APR-01.  
DR PDB; 1JGM; 04-JUL-01.  
DR PDB; 1PSC; 01-APR-97.

DR PDB; 1PTA; 01-DEC-95.  
 DR InterPro; IPR000437; Prok\_lipoprot\_S.  
 DR InterPro; IPR001559; PTE.  
 DR Pfam; PF02126; PTE; 1.  
 DR PROSITE; PS01322; PHOSPHOTRIESTERASE\_1; 1.  
 DR PROSITE; PS01323; PHOSPHOTRIESTERASE\_2; 1.  
 KW Hydrolase; Membrane; Plasmid; Signal; Metal-binding; Zinc;  
 KW 3D-structure.  
 FT SIGNAL 1 29  
 FT CHAIN 30 365 PARATHION HYDROLASE.  
 FT METAL 55 55 ZINC 1.  
 FT METAL 57 57 ZINC 1.  
 FT METAL 169 169 ZINC 1 AND 2.  
 FT METAL 201 201 ZINC 2.  
 FT METAL 230 230 ZINC 2.  
 FT METAL 301 301 ZINC 1.  
 FT STRAND 36 39  
 FT TURN 40 41  
 FT STRAND 42 45  
 FT HELIX 46 49  
 FT STRAND 51 56  
 FT STRAND 59 60  
 FT TURN 63 64  
 FT HELIX 65 68  
 FT HELIX 70 73  
 FT HELIX 76 92  
 FT TURN 93 94  
 FT STRAND 95 100  
 FT HELIX 104 106  
 FT TURN 107 107  
 FT HELIX 110 120  
 FT TURN 121 121  
 FT STRAND 123 125  
 FT STRAND 127 129  
 FT HELIX 136 139  
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 FT HELIX 143 155  
 FT TURN 156 156  
 FT STRAND 158 158  
 FT TURN 159 162  
 FT STRAND 163 163  
 FT STRAND 167 171  
 FT HELIX 178 194  
 FT STRAND 198 201  
 FT HELIX 204 206  
 FT TURN 207 207  
 FT HELIX 208 218  
 FT TURN 219 220  
 FT HELIX 223 225  
 FT STRAND 226 228  
 FT HELIX 231 233  
 FT HELIX 237 246  
 FT TURN 247 247  
 FT STRAND 249 252  
 FT TURN 255 256  
 FT TURN 260 261  
 FT TURN 263 264

FT	HELIX	266	272
FT	HELIX	277	289
FT	TURN	290	291
FT	HELIX	293	295
FT	STRAND	296	298
FT	STRAND	305	306
FT	TURN	311	312
FT	HELIX	313	320
FT	TURN	322	323
FT	HELIX	324	326
FT	HELIX	327	330
FT	TURN	331	331
FT	HELIX	332	338
FT	TURN	339	340
FT	HELIX	343	350
FT	TURN	351	351
FT	HELIX	352	358
SQ	SEQUENCE	365 AA;	39003 MW; 41FF8E4B029B46DC CRC64;

Query Match 99.7%; Score 1693; DB 1; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-128;  
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	SIGTGDRINTVRGPITISEAGFTLT	THEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR	61	
Db	30	SIGTGDRINTVRGPITISEAGFTLT	THEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR	89	
Qy	62	ARAAGVRTIVDVSTFDIGRDVSLLAEV	SRAADVHI	VAATGLWFDPLSMRLRSVEELTQF	121
Db	90	ARAAGVRTIVDVSTFDIGRDVSLLAEV	SRAADVHI	VAATGLWFDPLSMRLRSVEELTQF	149
Qy	122	FLREIQYGIEDTGIRAGI	I KVATTGKATPFQELVLKAA	ARASLATGVPVTTHTAASQRDG	181
Db	150	FLREIQYGIEDTGIRAGI	I KVATTGKATPFQELVLKAA	ARASLATGVPVTTHTAASQRDG	209
Qy	182	EQQAAIFESEGLSPSRVCIGHSD	DDTDDLSYLTAARGY	LIGLDHIPHSAGLEDNASAS	241
Db	210	EQQAAIFESEGLSPSRVCIGHSD	DDTDDLSYLTAARGY	LIGLDHIPHSAGLEDNASAS	269
Qy	242	ALLGIRSWQTRALLIKALIDQGYM	KQILVSNDWLFGFSSYVTNIMDVMDRVNP	PDGMAFIP	301
Db	270	ALLGIRSWQTRALLIKALIDQGYM	KQILVSNDWLFGFSSYVTNIMDVMDRVNP	PDGMAFIP	329
Qy	302	LRVIPFLREKGVPQETLAGITVTN	PARFLSPTLRAS	337	
Db	330	LRVIPFLREKGVPQETLAGITVTN	PARFLSPTLRAS	365	